E. Saoud

1646

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/065,330B

DATE: 06/05/2000
TIME: 11:38:12

Input Set : A:\Sequence.Lst.txt
Output Set: N:\CRF3\06022000\I065330B.raw

Does Not Comply
Corrected Diskette Needed

pp 1-3

```
 3 <110> APPLICANT: Walker, Ameae M.
 5 <120> TITLE OF INVENTION: PROLACTIN ANTAGONISTS AND USES THEREOF
 7 <130> FILE REFERENCE: Walker_2500_097US2
 9 <140> CURRENT APPLICATION NUMBER: 09/065,330B
10 <141> CURRENT FILING DATE: 1998-04-23
12 <150> PRIOR APPLICATION NUMBER: PCT/US97/01435
13 <151> PRIOR FILING DATE: 1997-01-30
15 <150> PRIOR APPLICATION NUMBER: 08/594,809
16 <151> PRIOR FILING DATE: 1996-01-31
18 <160> NUMBER OF SEQ ID NOS: 6
20 <170> SOFTWARE: PatentIn Ver. 2.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 832
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
27 <220> FEATURE:
28 <221> NAME/KEY: mutation
29 <222> LOCATION: (622)..(624)
30 <223> OTHER INFORMATION: This is the codon for the substituted amino acids
31       of the mutated sequence.
33 <400> SEQUENCE: 1
34 aacatgaaca tcaaaggatc gccatggaaa gggtccctcc tgctgctgct ggtgtcaaac 60
35 ctgctgctgt gccagagcgt ggcccccttg cccatctgtc ccggcggggc tgcccgatgc 120
36 caggtgaccc ttcgagacct gtttgaccgc gccgtcgtcc tgtcccacta catccataac 180
37 ctctcctcag aaatgttcag cgaattcgat aaacggtata cccatggccg ggggttcatt 240
38 accaaggcca tcaacagctg ccacacttct tcccttgcca cccccgaaga caaggagcaa 300
39 gcccaacaga tgaatcaaaa agactttctg agcctgatag tcagcatatt gcgatcctgg 360
40 aatgagcctc tgtatcatct ggtcacggaa gtacgtggta tgcaagaagc cccggaggct 420
41 atcctatcca aagctgtaga gattgaggag caaaccaaac ggcttctaga gggcatggag 480
42 ctgatagtca gccaggttca tcctgaaacc aaagaaaatg agatctaccc tgtctggtcg 540
43 ggacttccat ccctgcagat ggctgatgaa gagtctcgcc tttctgctta ttataacctg 600
44 ctccactgcc tacgcaggga tnnncataaa atcgacaatt atctcaagct cctgaagtgc 660
45 cgaatcatcc acaacaacaa ctgctaagcc cacatccatt tcatctattt ctgagaaggt 720
46 ccttaatgat ccgttccatt gcaagcttct tttagttgta tctcttttga atccatgctt 780
47 gggtgtaaca ggtctcctct taaaaaataa aaactgactc gttagagaca tc 832
51 <210> SEQ ID NO: 2
52 <211> LENGTH: 228
53 <212> TYPE: PRT
54 <213> ORGANISM: Homo sapiens
56 <220> FEATURE:
57 <221> NAME/KEY: VARIANT
58 <222> LOCATION: (208)
59 <223> OTHER INFORMATION: Site mutated codon where the normal codon coding
60       for serine is modified preferably to encode for
61       aspartate or glutamate, most preferably aspartate.
63 <400> SEQUENCE: 2
64 Asn Met Asn Ile Lys Gly Ser Pro Trp Lys Gly Ser Leu Leu Leu Leu
```

? a codon consists of three bases

```
                           5                      10                     15
65    1
67 Leu Val Ser Asn Leu Leu Leu Cys Gln Ser Val Ala Pro Leu Pro Ile
68                  20                      25                     30
70 Cys Pro Gly Gly Ala Ala Arg Cys Gln Val Thr Leu Arg Asp Leu Phe
71       35                      40                     45
73 Asp Arg Ala Val Val Leu Ser His Tyr Ile His Asn Leu Ser Ser Glu
74    50                      55                     60
76 Met Phe Ser Glu Phe Asp Lys Arg Tyr Thr His Gly Arg Gly Phe Ile
77    65                      70                     75                80
79 Thr Lys Ala Ile Asn Ser Cys His Thr Ser Ser Leu Ala Thr Pro Glu
80                  85                      90                     95
82 Asp Lys Glu Gln Ala Gln Gln Met Asn Gln Lys Asp Phe Leu Ser Leu
83                  100                     105                    110
85 Ile Val Ser Ile Leu Arg Ser Trp Asn Glu Pro Leu Tyr His Leu Val
86       115                     120                    125
88 Thr Glu Val Arg Gly Met Gln Glu Ala Pro Glu Ala Ile Leu Ser Lys
89    130                     135                    140
91 Ala Val Glu Ile Glu Glu Gln Thr Lys Arg Leu Leu Glu Gly Met Glu
92 145                     150                    155                160
94 Leu Ile Val Ser Gln Val His Pro Glu Thr Lys Glu Asn Glu Ile Tyr
95                  165                     170                    175
97 Pro Val Trp Ser Gly Leu Pro Ser Leu Gln Met Ala Asp Glu Glu Ser
98                  180                     185                    190
W--> 101 Arg Leu Ser Ala Tyr Tyr Asn Leu Leu His Cys Leu Arg Arg Asp Xaa
102             195                     200                    205
104 His Lys Ile Asp Asn Tyr Leu Lys Leu Leu Lys Cys Arg Ile Ile His
105       210                     215                    220
107 Asn Asn Asn Cys
108 225
112 <210> SEQ ID NO: 3
113 <211> LENGTH: 23
114 <212> TYPE: DNA
115 <213> ORGANISM: Artificial Sequence
117 <220> FEATURE:
118 <223> OTHER INFORMATION: Description of Artificial Sequence: This sequence
119       is a primer.
121 <400> SEQUENCE: 3
122 gcagggatga ccacaaggtt gac                                        23
125 <210> SEQ ID NO: 4
126 <211> LENGTH: 24
127 <212> TYPE: DNA
128 <213> ORGANISM: Artificial Sequence
130 <220> FEATURE:
131 <223> OTHER INFORMATION: Description of Artificial Sequence: This sequence
132       is a primer.
134 <220> FEATURE:
135 <221> NAME/KEY: variation
136 <222> LOCATION: (12)
137 <223> OTHER INFORMATION: This is a codon that can be replaced for nucleic
```

[handwritten note] a codon consists of three bases — location 12 "n" is only one

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/065,330B

DATE: 06/05/2000
TIME: 11:38:12

Input Set : A:\Sequence.Lst.txt
Output Set: N:\CRF3\06022000\I065330B.raw

```
     138        acid substitutes.                                                    24
     140 <400> SEQUENCE: 4
W--> 141 cgcaagggat gcacacaagg ttga
     144 <210> SEQ ID NO: 5
     145 <211> LENGTH: 22
     146 <212> TYPE: DNA
     147 <213> ORGANISM: Artificial Sequence
     151 <220> FEATURE:
     152 <223> OTHER INFORMATION: Description of Artificial Sequence: This sequence
     153        is a primer.
     155 <220> FEATURE:
     156 <221> NAME/KEY: variation
     157 <222> LOCATION: (12)
     158 <223> OTHER INFORMATION: This is a codon that can be replaced for nucleic
     159        acid substitutes.
     161 <400> SEQUENCE: 5                                                           22
W--> 162 acgcagggat gkataaaat cg
     165 <210> SEQ ID NO: 6
     166 <211> LENGTH: 26
     167 <212> TYPE: DNA
     168 <213> ORGANISM: Artificial Sequence
     170 <220> FEATURE:
     171 <223> OTHER INFORMATION: Description of Artificial Sequence: This sequence
     172        is a primer.
     174 <400> SEQUENCE: 6                                                           26
     175 cgtggccccc atatgttgcc catctg
W--> 178 4
```

same error

delete at end of file

6/5/00

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/065,330B

DATE: 06/05/2000
TIME: 11:38:13

Input Set : A:\Sequence.Lst.txt
Output Set: N:\CRF3\06022000\I065330B.raw

L:44 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:101 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:141 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:162 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:178 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6